Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _09/830,706_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

```
RAW SEQUENCE LISTING              DATE: 05/18/2001
PATENT APPLICATION:  US/09/830,706    TIME: 10:56:57

        Input Set : A:\M3-007PCT_SEQ.txt
        Output Set: N:\CRF3\05182001\I830706.raw
```

Does Not Comply
Corrected Diskette Needed

ppl-2 13

```
   4 <110> APPLICANT: Medical & Biological Laboratories Co.,Ltd.
   7 <120> TITLE OF INVENTION: Thioredoxin reductase II
  10 <130> FILE REFERENCE: M3-007PCT
  12 <140> CURRENT APPLICATION NUMBER: US/09/830,706
  13 <141> CURRENT FILING DATE: 2001-04-27
  15 <150> PRIOR APPLICATION NUMBER: JP 1998-310422
  16 <151> PRIOR FILING DATE: 1998-10-30
  18 <160> NUMBER OF SEQ ID NOS: 37
  20 <170> SOFTWARE: PatentIn Ver. 2.0
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OK → (annotations beside lines 12, 13)

ERRORED SEQUENCES

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 451 <210> SEQ ID NO: 4
 452 <211> LENGTH: 492    494 (p.2)
 453 <212> TYPE: PRT
 454 <213> ORGANISM: Homo sapiens       <220>  ← insert this mandatory
 455 <223> OTHER INFORMATION: Xaa(493) means selenosysteine.   numeric
 457 <400> SEQUENCE: 4                                          identifier
 458 Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly   whenever <221>,
 459   1               5                  10                  15        <222>, or <223>
 461 Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly   is shown
 462           20                  25                  30
 464 Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr   (Please correct
 465       35                  40                  45                   all sequences
 467 Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys   showing this
 468     50                  55                  60                     error.)
 470 Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala
 471  65                  70                  75                  80
 473 Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg
 474             85                  90                  95
 476 Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly
 477         100                 105                 110
 479 His Arg Val Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys
 480         115                 120                 125
 482 Ala Ser Phe Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly
 483     130                 135                 140
 485 Lys Glu Ile Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly
 486 145                 150                 155                 160
 488 Arg Pro Arg Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile
 489             165                 170                 175
 491 Thr Ser Asp Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu
 492         180                 185                 190
 494 Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr
 495         195                 200                 205
 497 Gly Ile Gly Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg
 498     210                 215                 220
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501 225                 230                 235                 240
503 His Gly Thr Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg
504                 245                 250                 255
506 Leu Pro Asp Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly
507                 260                 265                 270
509 Lys Glu Asp Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg
510             275                 280                 285
512 Val Pro Asp Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr
513         290                 295                 300
515 Ser Pro Asp Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser
516 305                 310                 315                 320
518 Val Pro His Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu
519                 325                 330                 335
521 Leu Thr Pro Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu
522                 340                 345                 350
524 Phe Gly Gly Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr
525         355                 360                 365
527 Val Phe Thr Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu
528         370                 375                 380
530 Ala Val Ala Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His
531 385                 390                 395                 400
533 Tyr Lys Pro Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys
534                 405                 410                 415
536 Tyr Val Lys Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly
537             420                 425                 430
539 Leu His Phe Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala
540             435                 440                 445
542 Leu Gly Ile Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val
543         450                 455                 460
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549                 485                 490
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937 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING   DATE: 05/18/2001
PATENT APPLICATION: US/09/830,706   TIME: 10:56:58

Input Set : A:\M3-007PCT_SEQ.txt
Output Set: N:\CRF3\05182001\I830706.raw

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RAW SEQUENCE LISTING              DATE: 05/18/2001
PATENT APPLICATION:  US/09/830,706    TIME: 10:56:58

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       Output Set: N:\CRF3\05182001\I830706.raw

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Output Set: N:\CRF3\05182001\I830706.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,706

DATE: 05/18/2001
TIME: 10:56:58

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Output Set: N:\CRF3\05182001\I830706.raw

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Please Note:
Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a c rresponding explanation is pres nted in the <220> to
<223> fields f each sequence which presents at least one n or Xaa.

RAW SEQUENCE LISTING   DATE: 05/18/2001
PATENT APPLICATION: US/09/830,706   TIME: 10:56:58

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Output Set: N:\CRF3\05182001\I830706.raw

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